


Estimating RMRs of synonymous codons from E. coli proteomic data

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 An abbreviated version of this protocol was published in Science Advances in Jul 2022

Preferred synonymous codons are translated more accurately: Proteomic evidence, among-species variation, and mechanistic basis

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Detailed protocol

Calculating RMR involves two steps:

1. Determine the absolute mistranslation rate for each codon by dividing the total intensity of mistranslated (dependent) peptides by the combined intensity of all peptides (dependent and base) mapped to the codon;
2. Obtain the codon's RMR by dividing its absolute mistranslation rate by the average absolute mistranslation rate for all codons encoding the same amino acid;

Note that we use preprocessed data from a previous publication by Mordret et al ("Systematic detection of amino acid substitutions in proteomes reveals mechanistic basis of ribosome errors and selection for translation fidelity"), which has already tabulated the intensity of dependent and base peptides for each codon at each site. If you are working with raw proteomic data, please refer to the pipeline from the original paper or other related papers (e.g., <https://www.biorxiv.org/content/10.1101/2022.10.11.511697v1>).

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Sun, M. and Zhang, J. (2023). Estimating RMRs of synonymous codons from E. coli proteomic data. Bio-protocol Preprint. [bio-protocol.org/prep2210](https://doi.org/10.1101/2023.04.17.535110).
2. Sun, M. and Zhang, J. (2022). Preferred synonymous codons are translated more accurately: Proteomic evidence, among-species variation, and mechanistic basis. Science Advances 8(27). DOI: [10.1126/sciadv.abl9812](https://doi.org/10.1126/sciadv.abl9812)

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